



SEQUENCE LISTING

<110> BARCHFELD, Gail
DEL GIUDICE, Giuseppe
RAPPUOLI, Rino

<120> DETOXIFIED MUTANTS OF BACTERIAL ADP RIBOSYLATING TOXINS
AS PARENTERAL ADJUVANTS

<130> 2302 1393 / PP01393.002

<140> 09/044,696

<141> 1998 03 18

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(708)

<220>

<223> Description of Artificial Sequence: wild-type Subunit
A from E. coli heat labile toxin

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aat ggc gac aga tta tac cgt gct gac tct aga ccc cca gat gaa ata	48
Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile	
1 5 10 15	
aaa cgt ttc cgg agt ctt atg ccc aga ggt aat gag tac ttc gat aga	96
Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg	
20 25 30	
gga act caa atg aat att aat ctt tat gat cac gcg aga gga aca caa	144
Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln	
35 40 45	
acc ggc ttt gtc aga tat gat gac gga tat gtt tcc act tct ctt agt	192
Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser	
50 55 60	
ttg aga agt gct cac tta gca gga cag tat ata tta tca gga tat tca	240
Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser	
65 70 75 80	
ctt act ata tat atc gtt ata gca aat atg ttt aat gtt aat gat gta	288
Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val	
85 90 95	
att agc gta tac agc cct cac cca tat gaa cag gag gtt tct gcg tta	336

50	55	60	
Leu Arg Ser Ala His	Leu Ala Gly Gln Tyr	Ile Leu Ser Gly Tyr Ser	
65	70	75	80
Leu Thr Ile Tyr	Ile Val Ile Ala Asn Met	Phe Asn Val Asn Asp Val	
	85	90	95
Ile Ser Val Tyr	Ser Pro His Pro Tyr Glu	Gln Glu Val Ser Ala Leu	
	100	105	110
Gly Gly Ile Pro Tyr	Ser Gln Ile Tyr Gly Trp	Tyr Arg Val Asn Phe	
	115	120	125
Gly Val Ile Asp Glu	Arg Leu His Arg Asn Arg	Glu Tyr Arg Asp Arg	
	130	135	140
Tyr Tyr Arg Asn Leu	Asn Ile Ala Pro Ala Glu	Asp Gly Tyr Arg Leu	
	145	150	155
Ala Gly Phe Pro Pro	Asp His Gln Ala Trp Arg	Glu Glu Pro Trp Ile	
	165	170	175
His His Ala Pro Gln	Gly Cys Gly Asp Ser Ser	Arg Thr Ile Thr Gly	
	180	185	190
Asp Thr Cys Asn Glu	Glu Thr Gln Asn Leu Ser	Thr Ile Tyr Leu Arg	
	195	200	205
Glu Tyr Gln Ser Lys	Val Lys Arg Gln Ile Phe	Ser Asp Tyr Gln Ser	
	210	215	220
Glu Val Asp Ile Tyr	Asn Arg Ile Arg Asp	Glu Leu	
	225	230	235

<210> 3

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(720)

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<223> Description of Artificial Sequence: wild-type CT
subunit A

<400> 3

aat gat gat aag tta tat	cgg gca gat tct aga cct cct	gat gaa ata	48
Asn Asp Asp Lys Leu Tyr	Arg Ala Asp Ser Arg Pro Pro	Asp Glu Ile	
1	5	10	15

aag cag tca ggt ggt ctt atg	cca aga gga cag agt gag tac ttt gac	96
Lys Gln Ser Gly Gly Leu Met	Pro Arg Gly Gln Ser Glu Tyr Phe Asp	

20										25					30					
cga ggt act caa atg aat atc aac ctt tat gat cat gca aga gga act	144																			
Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr																				
35 40 45																				
cag acg gga ttt gtt agg cac gat gat gga tat gtt tcc acc tca att	192																			
Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile																				
50 55 60																				
agt ttg aga agt gcc cac tta gtg ggt caa act ata ttg tct ggt cat	240																			
Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His																				
65 70 75 80																				
tct act tat tat ata tat gtt ata gcc act gca ccc aac atg ttt aac	288																			
Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn																				
85 90 95																				
gtt aat gat gta tta ggg gca tac agt cct cat cca gat gaa caa gaa	336																			
Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu																				
100 105 110																				
gtt tct gct tta ggt ggg att cca tac tcc caa ata tat gga tgg tat	384																			
Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr																				
115 120 125																				
cga gtt cat ttt ggg gtg ctt gat gaa caa tta cat cgt aat agg ggc	432																			
Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly																				
130 135 140																				
tac aga gat aga tat tac agt aac tta gat att gct cca gca gca gat	480																			
Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp																				
145 150 155 160																				
ggg tat gga ttg gca ggt ttc cct ccg gag cat aga gct tgg agg gaa	528																			
Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu																				
165 170 175																				
gag ccg tgg att cat cat gca ccg ccg ggt tgt ggg aat gct cca aga	576																			
Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg																				
180 185 190																				
tca tcg atc agt aat act tgc gat gaa aaa acc caa agt cta ggt gta	624																			
Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val																				
195 200 205																				
aaa ttc ctt gac gaa tac caa tct aaa gtt aaa aga caa ata ttt tca	672																			
Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser																				
210 215 220																				
ggc tat caa tct gat att gat aca cat aat aga att aag gat gaa tta	720																			
Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu																				
225 230 235 240																				
tga	723																			

<210> 4
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: wild-type CT
 subunit A

<400> 4
 Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
 1 5 10 15
 Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
 20 25 30
 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
 35 40 45
 Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
 50 55 60
 Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
 65 70 75 80
 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
 85 90 95
 Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
 100 105 110
 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
 115 120 125
 Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
 130 135 140
 Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
 145 150 155 160
 Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
 165 170 175
 Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
 180 185 190
 Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
 195 200 205
 Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
 210 215 220
 Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
 225 230 235 240